A1

Table IV

No	first adaptor	second adaptor	Corresponding primers
1*	5'-CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGT-3' (SEQ ID NO:1) 5'- ACCTGCCCGG-3' (SEQ ID NO:2)	5'-CTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAGGT-3' (SEQ ID NO:3) 5'- ACCTCGGCCG-3' (SEQ ID NO:4)	5'-CTAATACGACTCACTATAGGGC-3' (SEQ ID NO:5); Nested PCR Primer 1: 5'-TCGAGCGGCCGCCCGGGCAGGT-3' (SEQ ID NO:6); Nested PCR Primer 2: 5'-AGCGTGGTCGCGGCCGAGGT-3 (SEQ ID NO:7)
2*	5'-TCGAGCGGCCGCCCGGGCAGGT-3' (SEQ ID NO:8) 5'- ACCTGCCCGG-3' (SEQ ID NO:9)	5'-AGCGTGGTCGCGGCCGAGGT-3' (SEQ ID NO:10) 5'- ACCTCGGCCG-3' (SEQ ID NO:11)	5'-TCGAGCGGCCGCCCGGGCAGGT-3' (SEQ ID NO:12) 5'-AGCGTGGTCGCGGCCGAGGT-3' (SEQ ID NO:13)

*partially double-stranded.

Please replace the paragraph beginning on page 49, line 31 with the following amended paragraph:

Following annealing, a 2-step (nested) PCR amplification was performed to isolate sequences of interest. In the first PCR reaction only molecules which different adapter sequences on each end are amplified exponentially by the adapter-specific primer PCR1. The number of PCR cycles needed to obtain sufficient amounts of amplicon for analysis depends on the experimental paradigm under investigation, and needs to be determined empirically by performing the PCR amplification procedure with different cycle numbers and analyzing amplicon yields (e.g., by agarose gel electrophoresis). In

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